Integrated genomic characterization of papillary thyroid carcinoma.

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Public Summary:
Papillary thyroid carcinoma (PTC) is the most common type of thyroid cancer. Here, we describe the genomic landscape of 496 PTCs. We observed a low frequency of somatic alterations (relative to other carcinomas) and extended the set of known PTC driver alterations to include EIF1AX, PPM1D, and CHEK2 and diverse gene fusions. These discoveries reduced the fraction of PTC cases with unknown oncogenic driver from 25% to 3.5%. Combined analyses of genomic variants, gene expression, and methylation demonstrated that different driver groups lead to different pathologies with distinct signaling and differentiation characteristics. Similarly, we identified distinct molecular subgroups of BRAF-mutant tumors, and multidimensional analyses highlighted a potential involvement of oncomiRs in less-differentiated subgroups. Our results propose a reclassification of thyroid cancers into molecular subtypes that better reflect their underlying signaling and differentiation properties, which has the potential to improve their pathological classification and better inform the management of the disease.

Scientific Abstract:
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